SEQUENZPROTOKOLL

<110> Degussa AG

<120> Neue für das lysR2-Gen kodierende Nukleotidsequenzen

<130> 000181 BT

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<170> PatentIn Ver. 2.1

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cctcgacctt gctatctatt gcttggctca tggagttcat catgcgccaa cagcaaatat 180

tagtaaaatg ttagaaatag ctgtttttga ttcactttgt gcatgtaggc t gtg acc 237
                                                          Met Thr
                                                            1

atg ggc aac gac ggc gga gac ctg cga atc gac gac cta cgc agc ttc 285
Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe
          5              10                  15

att tca gtc gct caa tca ggc cac ctc acc gaa act gcc gaa aga tta 333
Ile Ser Val Ala Gln Ser Gly His Leu Thr Glu Thr Ala Glu Arg Leu
      20                  25                  30

ggc atc ccg cag ccc aca ctt tcc aga cga atc agc cga gtg gaa aaa 381
Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys
  35                  40              45                  50

cac gca ggc acc cca ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc 429
His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
                  55              60                  65

aac caa cga ggc cac gcc ttc ctc aac cac gcc agc gcc atc gtc gca 477
Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala
              70                  75                  80

gaa ttc aac tcc gcc gca act gaa atc aaa cgc ctc atg gac cca gaa 525
Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu
          85                  90                  95
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aaa ggc aca atc cga ctg gac ttc atg cat tcc ttg ggc act tgg atg    573
Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met
    100             105             110

gtc ccc gaa ctt atc cga aca ttc cgc gcc gaa cac ccc aac gta gaa    621
Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu
115             120             125             130

ttc caa ctc cac caa gcg gca gca atg ctc ctg gta gat cgt gtt ttg    669
Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu
            135             140             145

gct gat gaa act gac ctc gca tta gtt ggc ccc aaa cct gcc gag gtt    717
Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val
            150             155             160

ggt acc tct tta ggg tgg gcg cca ctg ctt cgt caa cga ctt gcc cta    765
Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu
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gct gtt ccc gca gat cac cgg ctt gcc tcc ttt tct ggc caa gga gaa    813
Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu
    180             185             190

ttg ccg ttg att act gcg gcg gaa gaa cct ttc gtg gcg atg cga gca    861
Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala
195             200             205             210

ggt ttc ggc acc cga ctc ctc atg gat gca tta gcc gaa gaa gcc ggt    909
Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly
            215             220             225

ttt gtt ccc aat gtg gtt ttc gaa tcc atg gaa ctc acc acc gtc gca    957
Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala
            230             235             240

ggg ctt gtc agc gca ggt ctc ggc gtt ggt gtg gtt ccg atg gat gat   1005
Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp
    245             250             255

ccg tac ctt ccc aca gtg gga atc gtg caa cgc cca ctt agt cca ccc   1053
Pro Tyr Leu Pro Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro
    260             265             270

gct tat agg gaa cta ggt ttg gtg tgg cga ctc aac gcg ggg ccg gca   1101
Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly Pro Ala
275             280             285             290

cct gcg gtg gat aac ttc cgg aag ttc gtg gcg gga tcg agg tat gca   1149
Pro Ala Val Asp Asn Phe Arg Lys Phe Val Ala Gly Ser Arg Tyr Ala
            295             300             305

tta gaa gag ggc tgagctgtaa gtgtcgtggg tgccgtttta agggggttgag   1201
Leu Glu Glu Gly
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ttttcccgat gactaggagt tggtccagat tgtgcgttag gggcccctag gggcgattct 1261
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Arg Leu Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val
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Glu Lys His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu
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Val Leu Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile
    65                  70                  75                  80

Val Ala Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp
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Pro Glu Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr
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Trp Met Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn
            115                 120                 125

Val Glu Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg
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Val Leu Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala
145                 150                 155                 160

Glu Val Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu
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Ala Leu Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln
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Gly Glu Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met
            195                 200                 205

Arg Ala Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu
        210                 215                 220

Ala Gly Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr
225                 230                 235                 240

Val Ala Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met
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        Asp Asp Pro Tyr Leu Pro Thr Val Gly Ile·Val Gln Arg Pro Leu Ser
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     5  Pro Pro Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly
                    275                 280             285

        Pro Ala Pro Ala Val Asp Asn Phe Arg Lys Phe Val Ala Gly Ser Arg
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    10  Tyr Ala Leu Glu Glu Gly
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        tccgaacatt ccgcgccgaa cacccaacg tagaattcca actccaccaa gcggcagcaa 180
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        ctgccgaggt tggtacctct ttagggtggg cgccactgct tcgtcaacga cttgccctag 300
        ctgttcccgc agatcaccgg cttgcctcct tttctggcca aggagaattg ccgttgatta 360
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        atgcattagc cgaagaagc                                              439
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